CLAIMS

We claim:

1. A method comprising:
    a. providing a composition comprising first primers and target nucleic acid, wherein either said first primers ro said target nucleic acid is immobilized to at least one solid support;
    b. performing a first analysis of said target nucleic acid, said first analysis comprising:
        i) contacting said first primers with said target nucleic acid whereby at least one of said first primers hybridizes with said target nucleic acid;
        ii) removing unhybridized first primers; and
        iii) contacting said hybridized first primers with an enzyme such that said hybridized first primers are modified forming first modified primers, whereby said target nucleic acid is not consumed; and
    c. performing a second analysis of said target nucleic acid.

2. The method according to claim 1 wherein said second analysis comprises:
    a. contacting second primers with said target nucleic acid whereby at least one of said second primers hybridizes with said target nucleic acid;
    b. removing unhybridized second primers; and
    c. contacting said hybridized second primers with an enzyme such that said hybridized second primers are modified forming second modified primers.

3. The method according to claim 2, further comprising detecting said first and second modified primers.

4. The method according to claim 2, further comprising amplifying said first and second modified primers to form first and second amplicons.

5. The method according to claim 4, further comprising detecting said first and second amplicons.

6. The method according to claim 5, wherein said first and second amplicons comprise labels.

7. The method according to claim 6, wherein said first and second amplicons are labeled during said amplification.

8. The method according to claim 1, wherein said target nucleic acid comprises genomic DNA.

9. The method according to claim 8, wherein said genomic DNA comprises at least one copy of the genomic DNA from an organism.

10. The method according to claim 9, wherein said organism is selected from humans, mice, pigs, cows, bacteria, viruses or plants.

11. The method according to claim 1, wherein at least one of said first and second primers comprises an adapter sequence.

12. A method comprising:

a. providing a composition comprising first primers and target nucleic acid wherein said first primers are ligation primers;

b. hybridizing said first ligation primers with said target nucleic acid to form first ligation complexes, whereby said first ligation primers hybridize to said target nucleic acid flanking a first target sequence;

c. removing unhybridized ligation primers;

d. contacting said first ligation complexes with a ligation enzyme, whereby when said first ligation primers are complementary to said first target sequences, said ligation enzyme ligates said first ligation primers generating first ligation products;

e. removing said first ligation products from said target nucleic acid;

f. hybridizing said target nucleic acid with second ligation primers to form second ligation complexes, whereby said second ligation primers hybridize to said target nucleic acid flanking a second target sequence;

g. contacting said second ligation complex with a ligation enzyme, whereby when said second ligation primers are complementary to said second target sequence, said ligation enzyme ligates said second ligation primers generating second ligation products.

13. The method according to claim 12 further comprising:

h. contacting said first and second ligation products with amplification primers, nucleotides and amplification enzyme to form first and second amplicons; and

i. detecting said first and second amplicons.

14. The method according to claim 13, wherein said amplification enzyme is a DNA polymerase and said nucleotides are dNTPs.

15. The method according to claim 13, wherein said amplification enzyme is an RNA polymerase and said nucleotides are NTPs.

16. A method of reusing target nucleic acid comprising:

a. providing a composition comprising first primers and target nucleic acid, wherein either said first primers or said target nucleic acid are immobilized on at least one solid support;

b. performing a first analysis of said target nucleic acid, said first analysis comprising: said first analysis comprising:

i) contacting said first primers with said target nucleic acid whereby at least one of said first primers hybridizes with said target nucleic acid;

ii) removing unhybridized first primers; and

iii) contacting said hybridized first primers with an enzyme such that said hybridized first primers are modified forming first modified primers,

whereby said target nucleic acid is not consumed whereby said target nucleic acid is not consumed; and

c. reusing said target nucleic acid in a second analysis.

17. The method according to claim 16, wherein said target nucleic acid is reused at least five times.

18. The method according to claims 12 or 16, wherein said target nucleic acid is genomic DNA.

19. The method according to claim 1, 12 or 16, wherein said target nucleic acid is immobilized on at least one solid support.

20. The method according to claim 1, 12 or 16, wherein said first primers are immobilized on at least one solid support.

21. the method according to claim 1, 12 or 16, wherein at least 10 different target nucleic acids are analyzed in a single reaction.

22. The method according to claim 1, 12 or 16, wherein at least 50 different target nucleic acids are analyzed in a single reaction.

23. The method according to claim 1, 12 or 16, wherein at least 100 different target nucleic acids are analyzed in a single reaction.